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OM nucleic - nucleic search, using sw model

Run on: January 22, 2007, 22:40:41 ; Search time 3879.36 Seconds
                                           (without alignments)
                                           9890.408 Million cell updates/sec

Title: US-10-750-622-4518
Perfect score: 599.6
Sequence: 1 aaattcttctcctcctctct..........cgcagcattaaaagagggcc 600

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
               1: gb_env:*
               2: gb_pat:*
               3: gb_ph:*
               4: gb_pl:*
               5: gb_pr:*
               6: gb_ro:*
               7: gb_sts:*
               8: gb_sy:*
               9: gb_un:*
               10: gb_vi:*
               11: gb_ov:*
               12: gb_htg:*
               13: gb_in:*
               14: gb_om:*
               15: gb_ba:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                       %
Result   Query
    No.   Score Match Length DB   ID   Description
----
c   1   598   99.7 269031 12   AC167224   AC167224 Bos tauru
c   2   295.8 49.3 182462 5   AC092669   AC092669 Homo sapi

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OM nucleic - nucleic search, using sw model

Run on: January 22, 2007, 22:50:21 ; Search time 7288.32 Seconds
                                                (without alignments)
                                                4603.475 Million cell updates/sec

Title: US-10-750-622-4518
Perfect score: 599.6
Sequence: 1 aaattcttctcctcctctct..........cgcagcattaaaagagggcc 600

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                 1: gb_est1:*
                 2: gb_est3:*
                 3: gb_est4:*
                 4: gb_est5:*
                 5: gb_est6:*
                 6: gb_htc:*
                 7: gb_est2:*
                 8: gb_est7:*
                 9: gb_est8:*
                 10: gb_est9:*
                 11: gb_gss1:*
                 12: gb_gss2:*
                 13: gb_gss3:*
                 14: gb_gss4:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.

                                 SUMMARIES
                          %
Result   Query
    No.   Score   Match Length DB   ID   Description
    ----
       1 156.4   26.1   476 11 AQ112913   AQ112913 CIT-HSP-2
       2 108.2   18.0   768 11 BZ265275   BZ265275 CH230-521
    c 3   79.4   13.2   718 11 BH092744   BH092744 RPCI-24-3

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OM nucleic - nucleic search, using sw model

Run on: January 22, 2007, 23:11:25 ; Search time 1764.48 Seconds
                                            (without alignments)
                                            4178.331 Million cell updates/sec

Title: US-10-750-622-4518
Perfect score: 599.6
Sequence: 1 aaattcttctcctcctctct..........cgcagcattaaaagagggcc 600

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA_Main:*
                 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
                 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
                 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
                 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
                 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
                 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
                 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
                 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
  No.   Score   Match Length DB   ID   Description
----
     1   599.6   100.0   600   10 US-10-750-185-4518   Sequence 4518, Ap

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OM nucleic - nucleic search, using sw model

Run on: January 22, 2007, 23:31:43 ; Search time 406.08 Seconds
                                                (without alignments)
                                                4304.212 Million cell updates/sec

Title: US-10-750-622-4518
Perfect score: 599.6
Sequence: 1 aaattcttctcctcctctct..........cgcagcattaaaagagggcc 600

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 3950299 seqs, 1456545396 residues

Total number of hits satisfying chosen parameters: 7900598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA_New:*
                 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
                 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
                 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
                 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                    SUMMARIES

| | | %
Query | | | | |
Result No.	Score	Match	Length	DB	ID	Description
1	295.8	49.3	137359	7	US-11-033-056A-36532	Sequence 36532, A
2	50.2	8.4	104262	7	US-11-033-056A-36220	Sequence 36220, A
3	48.8	8.1	71638	7	US-11-033-056A-38193	Sequence 38193, A
c 4	48.6	8.1	225734	6	US-10-669-920-1137	Sequence 1137, Ap
c 5	47.6	7.9	685	6	US-10-956-160-8176	Sequence 8176, Ap
c 6	47.6	7.9	685	6	US-10-956-160-218283	Sequence 218283,

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OM nucleic - nucleic search, using sw model

Run on: January 22, 2007, 22:50:21 ; Search time 303.68 Seconds
                                             (without alignments)
                                             4603.475 Million cell updates/sec

Title: US-10-750-622-5719
Perfect score: 25
Sequence: 1 aacacactgggacatgctcgcattc 25

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                  1: gb_est1:*
                  2: gb_est3:*
                  3: gb_est4:*
                  4: gb_est5:*
                  5: gb_est6:*
                  6: gb_htc:*
                  7: gb_est2:*
                  8: gb_est7:*
                  9: gb_est8:*
                  10: gb_est9:*
                  11: gb_gss1:*
                  12: gb_gss2:*
                  13: gb_gss3:*
                  14: gb_gss4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                    SUMMARIES
                         %
Result   Query
    No.   Score   Match Length DB   ID   Description
    ----
    c   1   20.2   80.8   436   2   BJ088219   BJ088219 BJ088219
        2   20.2   80.8   470   2   BG348022   BG348022 de72h07.y
    c   3   20.2   80.8   628   2   BJ083957   BJ083957 BJ083957

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OM nucleic - nucleic search, using sw model

Run on: January 22, 2007, 22:40:41 ; Search time 161.64 Seconds
                                             (without alignments)
                                             9890.408 Million cell updates/sec

Title: US-10-750-622-5719
Perfect score: 25
Sequence: 1 aacacactgggacatgctcgcattc 25

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                 1: gb_env:*
                 2: gb_pat:*
                 3: gb_ph:*
                 4: gb_pl:*
                 5: gb_pr:*
                 6: gb_ro:*
                 7: gb_sts:*
                 8: gb_sy:*
                 9: gb_un:*
                 10: gb_vi:*
                 11: gb_ov:*
                 12: gb_htg:*
                 13: gb_in:*
                 14: gb_om:*
                 15: gb_ba:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
      1   25 100.0 199890 12 AC168938   AC168938 Bos tauru
      2   21.8   87.2 209895   5 AC074391   AC074391 Homo sapi

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: January 22, 2007, 23:31:43 ; Search time 16.92 Seconds
                                              (without alignments)
                                              4304.212 Million cell updates/sec

Title: US-10-750-622-5719
Perfect score: 25
Sequence: 1 aacacactgggacatgctcgcattc 25

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 3950299 seqs, 1456545396 residues

Total number of hits satisfying chosen parameters: 7900598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA_New:*
                1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
                9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
                10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
                11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

			% Query				
Result	No.	Score	Match	Length	DB	ID	Description
	1	18.2	72.8	315	8	US-11-217-529-75582	Sequence 75582, A
c	2	18.2	72.8	482767	7	US-11-033-056A-38391	Sequence 38391, A
c	3	18.2	72.8	486468	7	US-11-033-056A-35962	Sequence 35962, A
c	4	18.2	72.8	507300	7	US-11-033-056A-36751	Sequence 36751, A
	5	17.8	71.2	1048668	7	US-11-033-056A-36314	Sequence 36314, A
	6	17.6	70.4	282	8	US-11-266-748A-409998	Sequence 409998,

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OM nucleic - nucleic search, using sw model

Run on: January 22, 2007, 23:11:25 ; Search time 73.52 Seconds
                                             (without alignments)
                                             4178.331 Million cell updates/sec

Title: US-10-750-622-5719
Perfect score: 25
Sequence: 1 aacacactgggacatgctcgcattc 25

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA_Main:*
                 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
                 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
                 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
                 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
                 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
                 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
                 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
                 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
   No.   Score Match Length DB   ID   Description
----
     1   25   100.0   25 10 US-10-750-185-5719   Sequence 5719, Ap